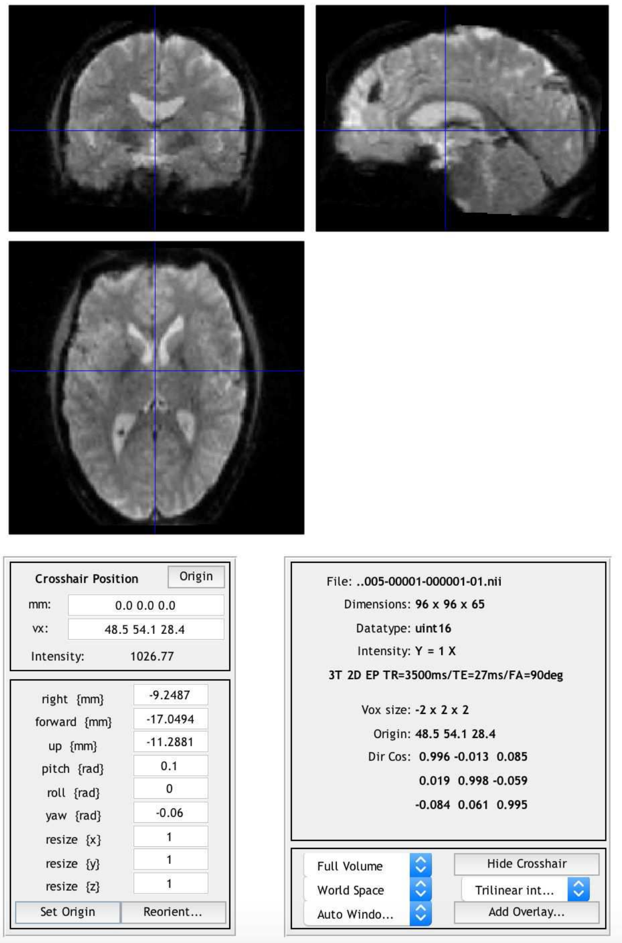
Portofolio 4

27/2 2020

Morten Street, Anders Hjulmand, Sigrid Bom & Gustav Helms

1. Intitial alignment of data to standard stereotachtic space (MNI-space)



Crosshair Position

mm: 0.0 0.0 0.0

vx: 48.5 54.1 28.4

Intensity: 1026.77

right {mm}	-9.2487
forward {mm}	-17.0494
up {mm}	-11.2881
pitch {rad}	0.1
roll {rad}	0
yaw {rad}	-0.06
resize {x}	1
resize {y}	1
resize {z}	1

File: ..005-00001-000001-01.nii

Dimensions: 96 x 96 x 65

Datatype: uint16

Intensity: Y = 1 X

3T 2D EP TR=3500ms/TE=27ms/FA=90deg

Vox size: -2 x 2 x 2

Origin: 48.5 54.1 28.4

Dir Cos: 0.996 -0.013 0.085
0.019 0.998 -0.059
-0.084 0.061 0.995

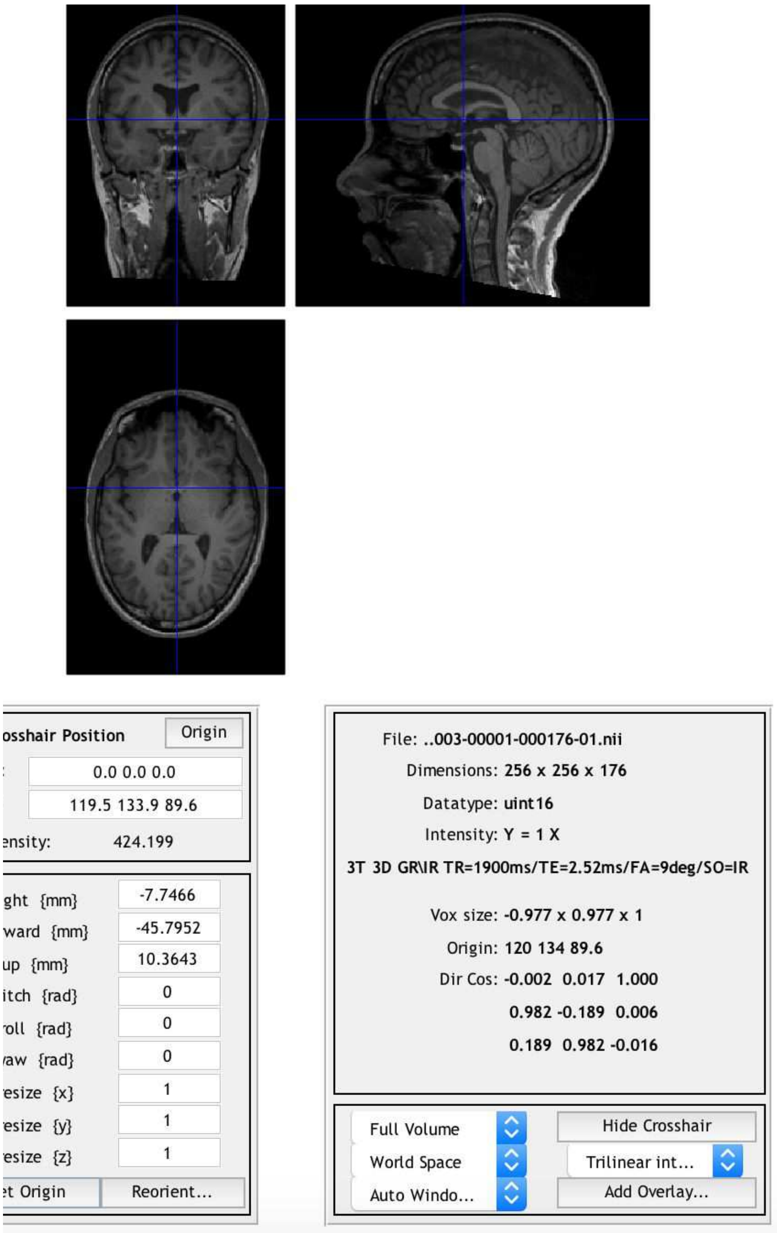
Full Volume

World Space

Auto Windo...

Trilinear int...

First functional image.



osshair Position Origin

: 0.0 0.0 0.0

119.5 133.9 89.6

ensity: 424.199

ght {mm} -7.7466

ward {mm} -45.7952

up {mm} 10.3643

itch {rad} 0

oll {rad} 0

aw {rad} 0

esize {x} 1

esize {y} 1

esize {z} 1

t Origin Reorient...

File: ..003-00001-000176-01.nii

Dimensions: 256 x 256 x 176

Datatype: uint16

Intensity: Y = 1 X

3T 3D GR\IR TR=1900ms/TE=2.52ms/FA=9deg/SO=IR

Vox size: -0.977 x 0.977 x 1

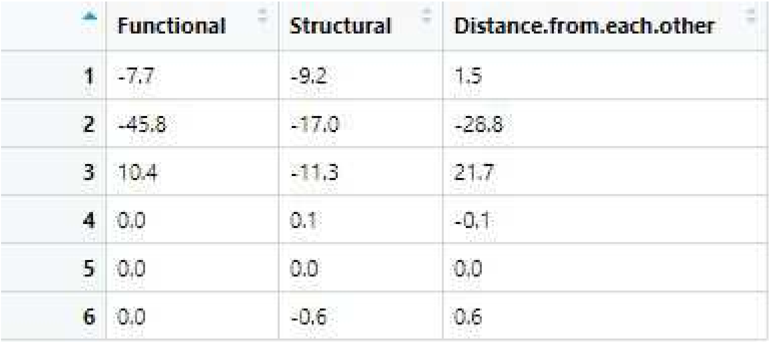
Origin: 120 134 89.6

Dir Cos: -0.002 0.017 1.000

0.982 -0.189 0.006

0.189 0.982 -0.016

Structual image.



	Functional	Structural	Distance.from.each.other
1	-7.7	-9.2	1.5
2	-45.8	-17.0	-28.8
3	10.4	-11.3	21.7
4	0.0	0.1	-0.1
5	0.0	0.0	0.0
6	0.0	-0.6	0.6

The first coloumn shows the realignment parameters (1-6) for the first functional image. The second coloumn shows the realignment parameters (1-6) for the single structural image. IN the last coloumn we see that the images are quite far from each other, especially in realignment parameter 2 and 3 (forward and up)

2. Preprocessing of fMRI data

Follow the example in the SPM12 manual chapter 30. Apply the same preprocessing procedure to the current data. This means:

2.a. realignment

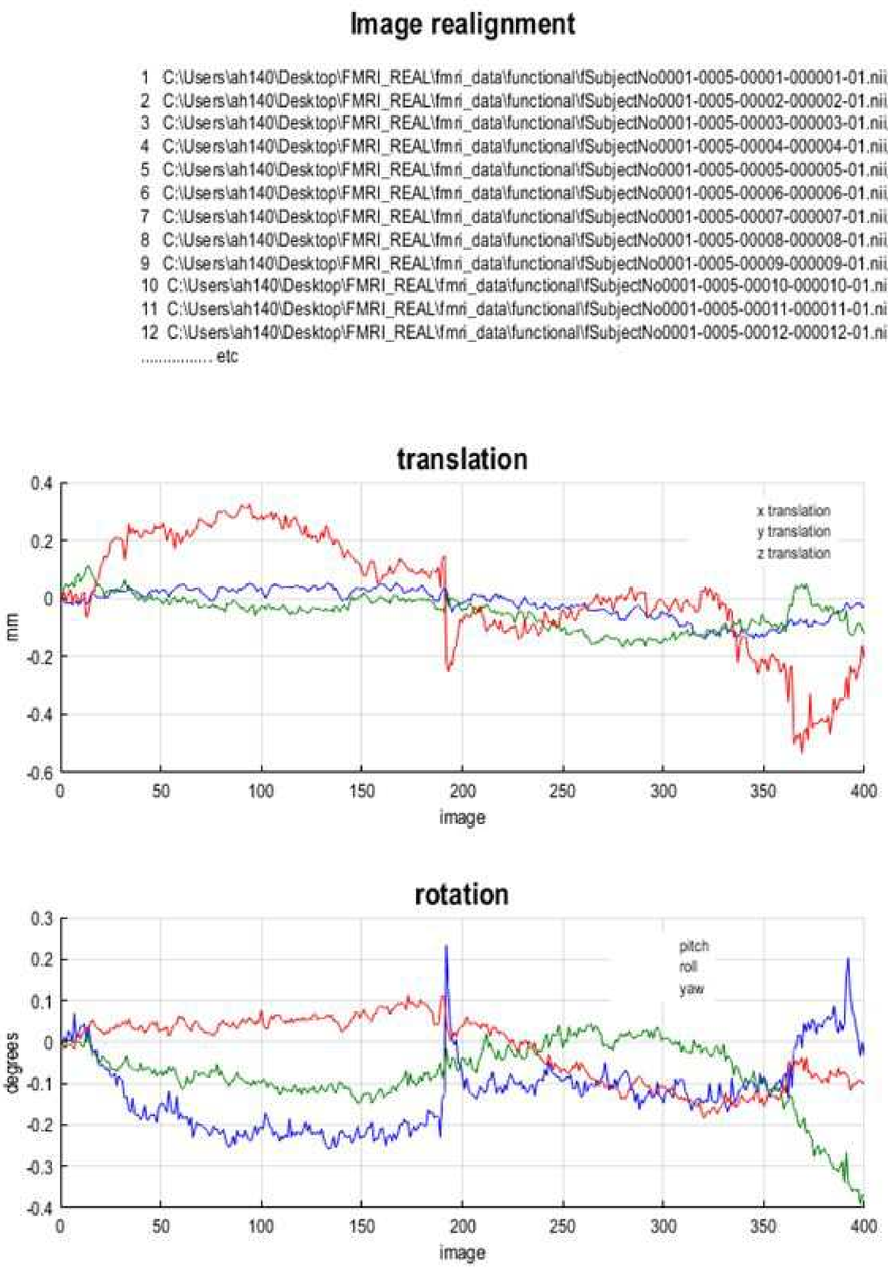
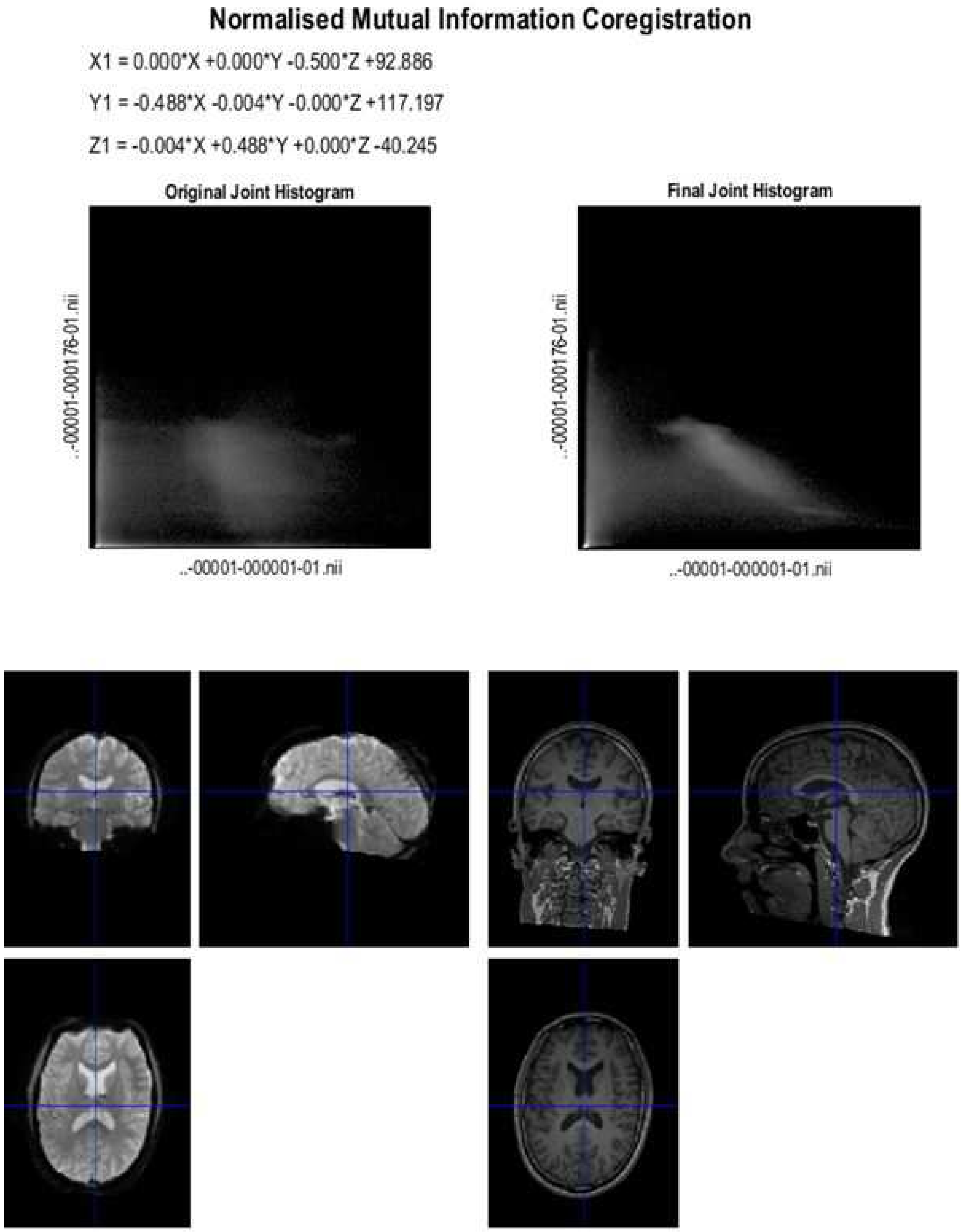


Image realignment

```
1  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00001-000001-01.nii,1
2  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00002-000002-01.nii,1
3  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00003-000003-01.nii,1
4  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00004-000004-01.nii,1
5  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00005-000005-01.nii,1
6  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00006-000006-01.nii,1
7  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00007-000007-01.nii,1
8  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00008-000008-01.nii,1
9  C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00009-000009-01.nii,1
10 C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00010-000010-01.nii,1
11 C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00011-000011-01.nii,1
12 C:\Users\ah140\Desktop\FMRI_REAL\fmri_data\functional\fSubjectNo0001-0005-00012-000012-01.nii,1
................ etc
```

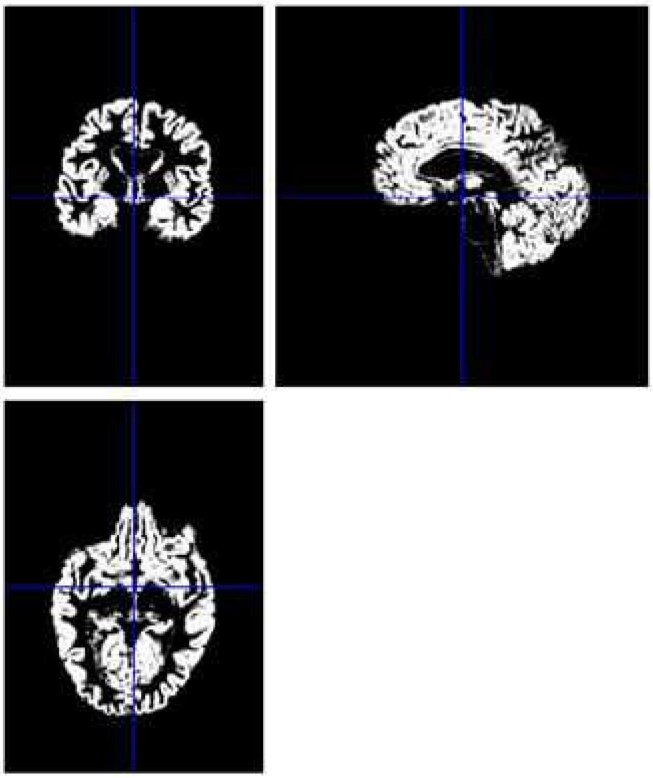
2.b. coregistration of function and structural data (hint: use “dependency” to point to the mean functional image),

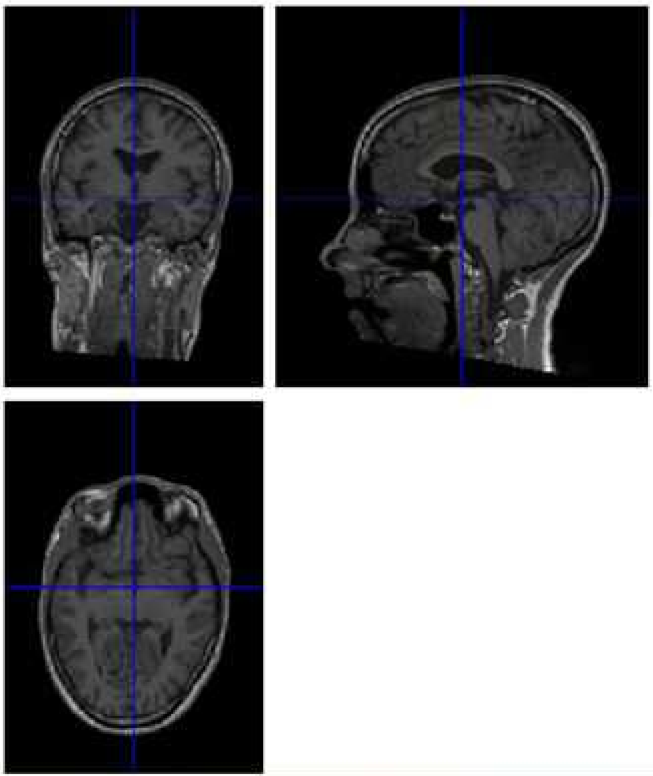


Normalised Mutual Information Coregistration

```
X1 = 0.000*X +0.000*Y -0.500*Z +92.886
Y1 = -0.488*X -0.004*Y -0.000*Z +117.197
Z1 = -0.004*X +0.488*Y +0.000*Z -40.245
```

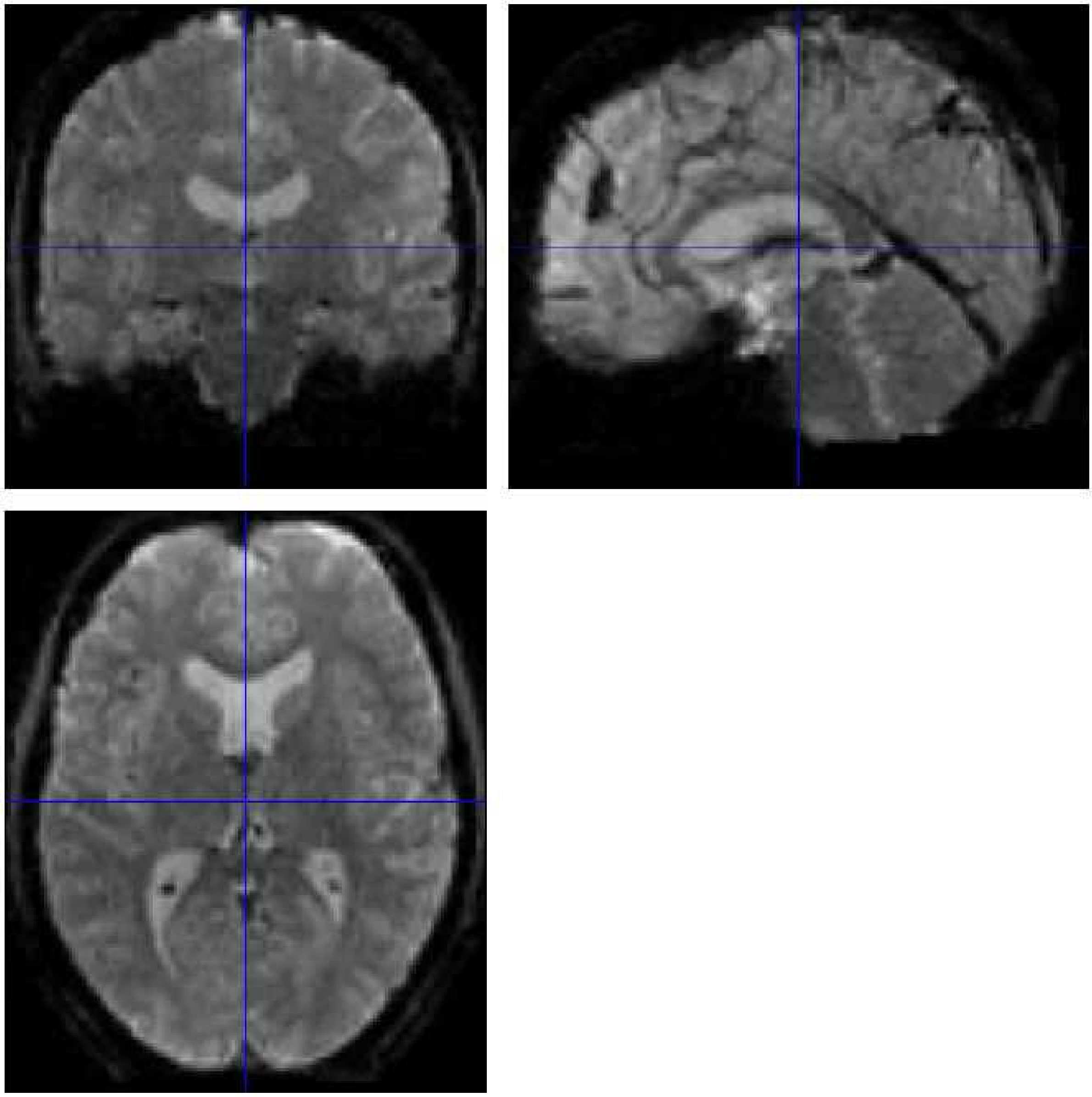
2.c. segmentation of structural data (again, use dependency to point the coregistered structural image)





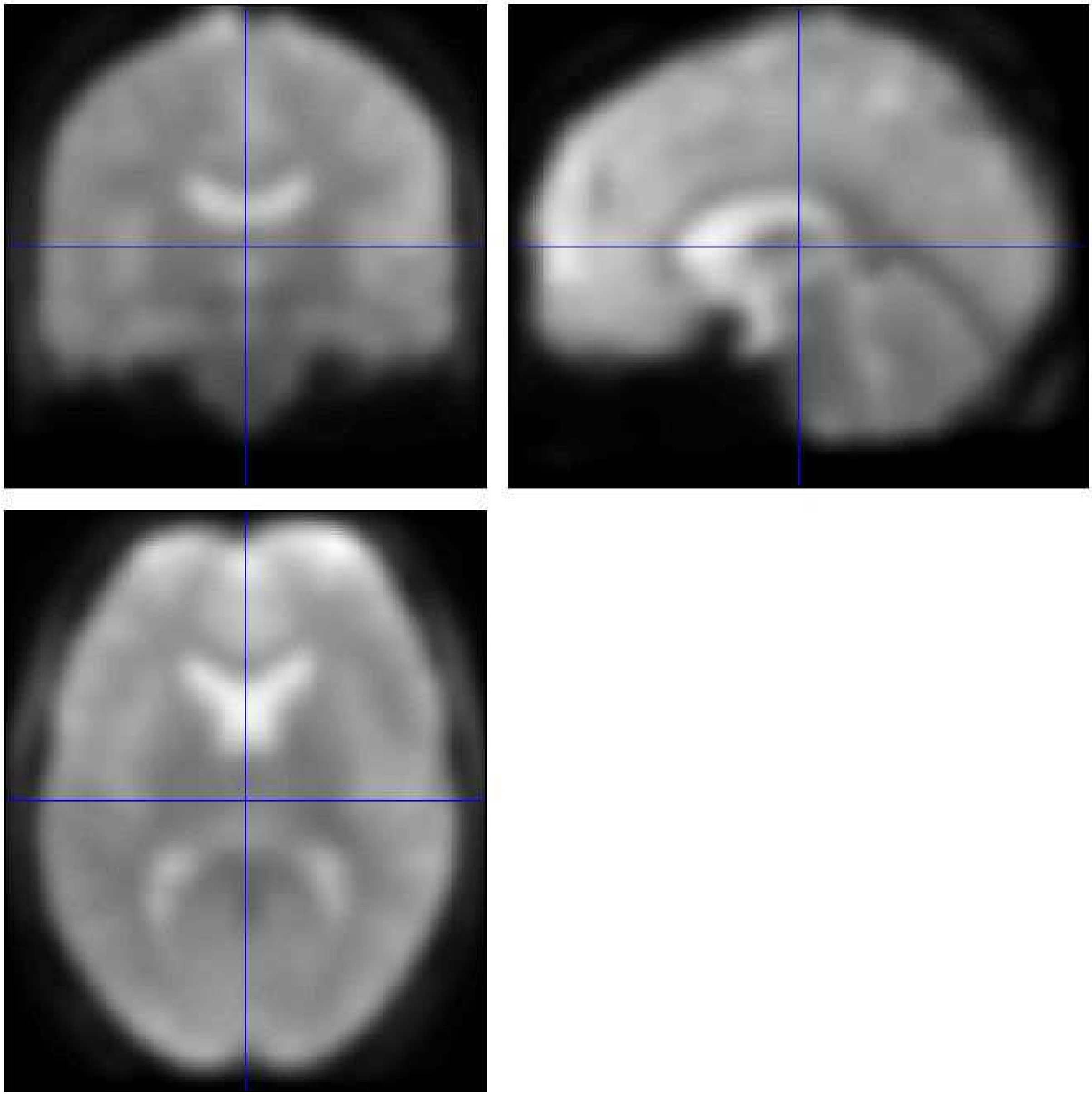
2.d. normalization using the forward deformation field from segmentation (hint: dependency and NB: No need to change voxel size), and

This is the first normalized functional image



2.e. smoothing (choose dependency and output from normalization) using a [8,8,8] mm FWHM gaussian kernel.

This is the first smoothed functional image



2.f. Save and report output from the graphics window for each step using the SPM figure menu. Use the “check reg.” button to show an example of a smoothed image (swf..nii) and save that as well.

Portofolio 4

Gustav Helmet, Morten Street, Anders Wheelman & Sigrid Snapfield

2/26/2020

```r
#Setup
library(pacman)
pacman::p_load("tidyverse", "lme4", "reshape2", "pracma","Hmisc")

#Importing data
alignment <- read.delim("alignment.txt", header = F, sep = "")

#Importing the designmatrix
fmrides<-as.matrix(read.csv("aud_fmri_design.csv", header=FALSE))
##making it a time-series
fmrides2<-ts(fmrides)
```

3. Realignment parameters

SPM produces a file with the realignment parameters, i.e. the calcultated participant movement and rotation per time point (called “rp. . . txt”, saved together with the functional data).

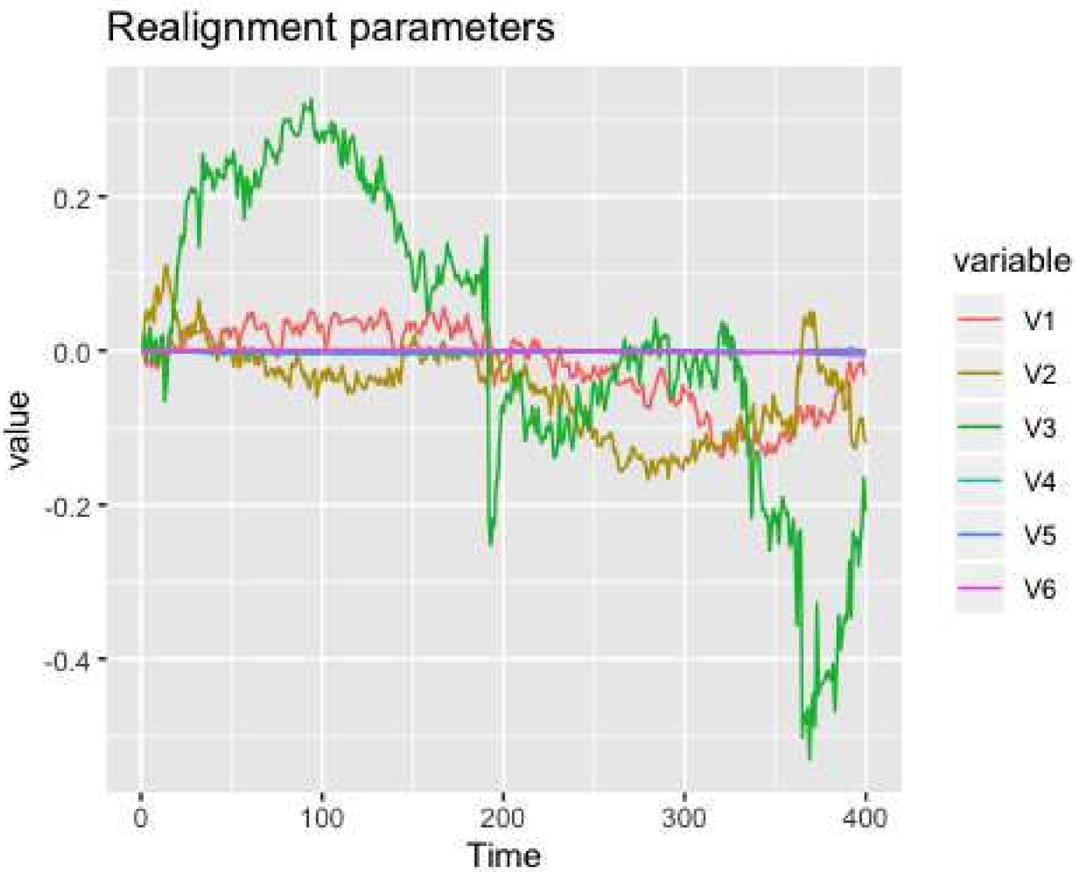
Import the realignment parameters into R.

3.a. Make a lineplot of the realignment parameters in R.

```r
#Transforming the dataframe into a melted format
alignment <- melt(alignment)
```

```
## No id variables; using all as measure variables
```

```r
#Making a new time variable for the x-axis
alignment$Time <- c(1:400)

#Plotting
ggplot(alignment, aes(Time, value, colour = variable))+
  geom_line()+
  ggtitle("Realignment parameters")
```



3.b. How far has the participant moved for each dimension during the experiment (Hint: use "apply()" to run a function across columns)?

```
#Converting all datapoints to absolute values and taking the sum of each
parameter
alignment %>% group_by(variable) %>% summarise(sum(sqrt(value^2)))
```

```
## # A tibble: 6 x 2
##   variable `sum(sqrt(value^2))`
##   <fct>                   <dbl>
## 1 V1                     17.5
## 2 V2                     23.8
## 3 V3                     62.6
## 4 V4                      0.953
## 5 V5                      0.574
## 6 V6                      0.485
```

3.c. Are any of the realignment parameters significantly correlated with the fMRI model (same model as used in exercise 3)?

```
#Transforming the data back from melted format and into a matrix
alignment <- read.delim("alignment.txt", header = F, sep = "")
alignment <- as.matrix(alignment)
```

```
#Making the correlation test between all variables
cor <- rcorr(alignment, fmrides, "spearman")

#Extracting the relevant values
cor <- data.frame("Rho_V1" = cor$r[1:6,7],
                 "p_value_V1" = cor$P[1:6,7],
                 "Significant_V1" = ifelse(cor$P[1:6,7]<0.05,"*"," "),
                 "Rho_V2" = cor$r[1:6,8],
                 "p_value_V2" = cor$P[1:6,8],
                 "Significant_V2" = ifelse(cor$P[1:6,8]<0.05,"*"," "))
cor
```

```
##          Rho_V1 p_value_V1 Significant_V1      Rho_V2 p_value_V2
## V1 -0.041909199  0.4031953                -0.07888110  0.1152241
## V2  0.043678605  0.3836154                 0.01670629  0.7390563
## V3  0.019339524  0.6997810                 0.01297360  0.7958893
## V4 -0.073960822  0.1397801                 0.10019205  0.0452190
## V5  0.088798454  0.0760769                 0.03154922  0.5292401
## V6 -0.005607653  0.9109797                -0.04839900  0.3342861
##    Significant_V2
## V1
## V2
## V3
## V4              *
## V5
## V6
```

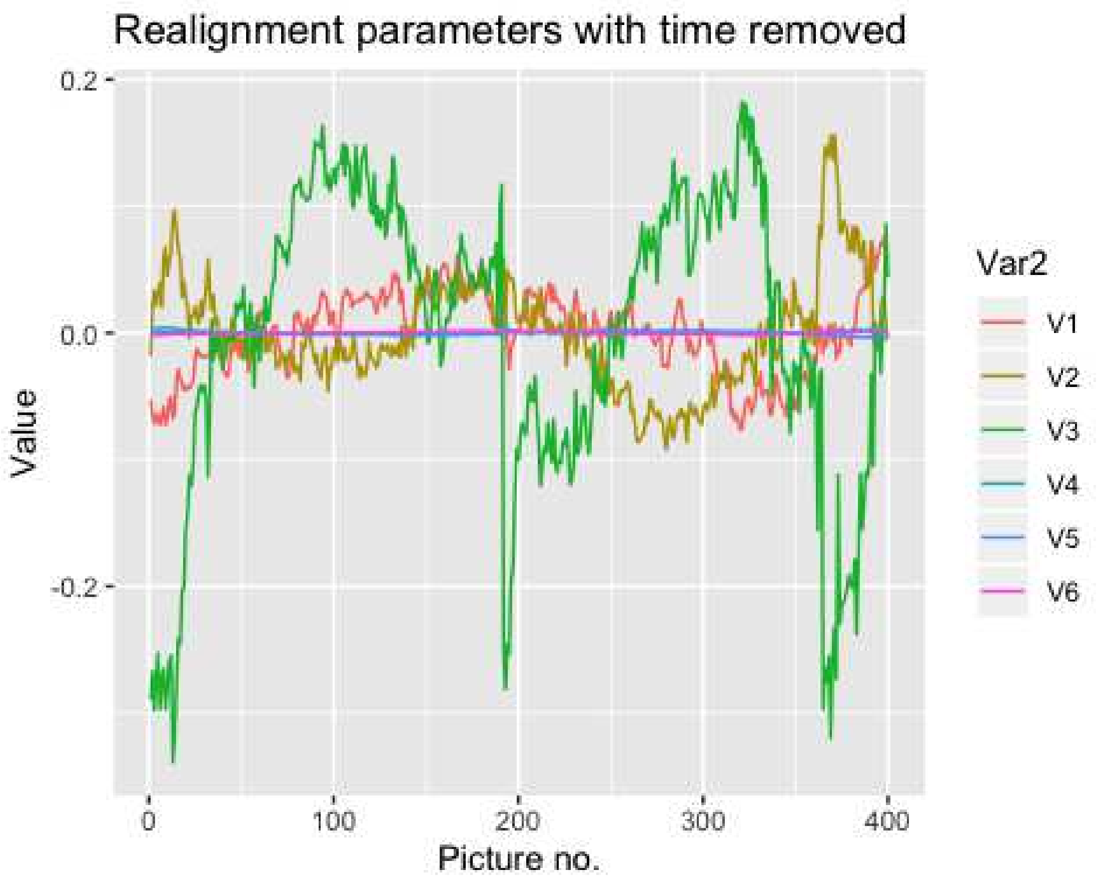
Realignment parameter 4 (pitch) is significantly correlated with the second model covariate, which most likely is due to chance.

Remove linear effects of time from the realignment parameters (hint: 1:400, fit a line and use residuals).

```
#Making a time vector
time <- c(1:400)

#Making a linear model
m <- lm(alignment~time)

#Encoding the residuals to matrix
residuals <- m$residuals
```

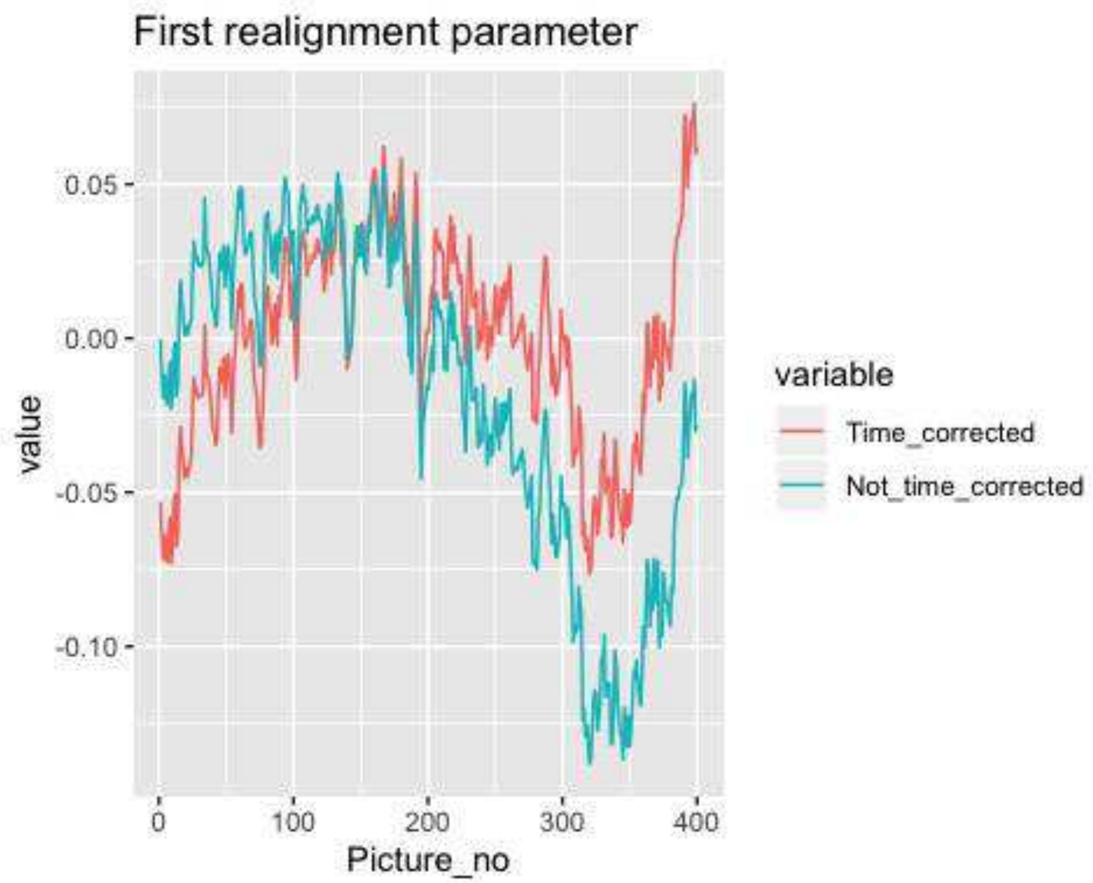
3.d. Make a lineplot of the realignment parameters with time removed.

```
#Converting to new format
melt_residuals <- melt(residuals)

#Making the lineplot
ggplot(melt_residuals, aes(Var1, value, colour = Var2))+
  geom_line()+
  labs(x = "Picture no.", y = "Value", title = "Realignment parameters with
time removed")
```



3.e. Make a lineplot including only the first realignment parameter before and after removal.

```
#Making a new data frame with the residuals and values of the first
parameter.
V1 <- data.frame("Time_corrected" = melt_residuals$value[melt_residuals$Var2
== "V1"],
                 "Not_time_corrected" = alignment[,1])

#Transforming the data frame into a new format
V1 <- melt(V1)

## No id variables; using all as measure variables

#Adding a variable for the x-axis
V1$Picture_no <- c(1:400)

#Plotting
ggplot(V1, aes(Picture_no, value, colour = variable))+
  geom_line()+
  ggtitle("First realignment parameter")
```



3.f. Are the realignment parameters (corrected for effects of time) now correlated with the fMRI model?

```
#Doing the correlation test like earlier
res_cor <- rcorr(residuals, fmrides, "spearman")

#Extracting the relevant correlation tests.
res <- data.frame("Rho_V1" = res_cor$r[1:6,7],
                  "p_value_V1" = res_cor$P[1:6,7],
                  "Significant_V1" = ifelse(res_cor$P[1:6,7]<0.05,"*"," "),
                  "Rho_V2" = res_cor$r[1:6,8],
                  "p_value_V2" = res_cor$P[1:6,8],
                  "Significant_V2" = ifelse(res_cor$P[1:6,8]<0.05,"*"," "))

res
```

```
##            Rho_V1 p_value_V1 Significant_V1       Rho_V2   p_value_V2
## V1 -0.0689742026  0.1685719                 -0.192119821 0.0001104317
## V2  0.0165235227  0.7418090                  0.005468536 0.9131792812
## V3  0.0006652631  0.9894175                 -0.036721460 0.4639379782
## V4 -0.0775218921  0.1216425                  0.103419103 0.0386912359
## V5  0.0831338250  0.0968444                  0.030906097 0.5376735888
## V6 -0.0291042628  0.5616540                 -0.098282645 0.0495000355
##    Significant_V2
## V1              *
## V2
## V3
## V4              *
## V5
## V6              *
```

There are 3 significant relations between the second covariate and the parameters. They are probably due to change, but the first p value at 0.00011 seems very unlikely to get by chance, so maybe there is an actual correlation?